

# SEQUENCE LISTING

<110> Larsen, Christian P.  
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Waller, Edmund K.  
Adams, Andrew B.

<120> METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND  
CORRECTING HEMOGLOBINOPATHIES

<130> D0136NP/30436.58USU1

<140> Not yet known  
<141> 2002-01-25

<150> 60/264,528  
<151> 2001-01-26

<150> 60/303,142  
<151> 2001-07-05

<160> 20

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1152  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: L104EIg  
sequence

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ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180  
acagtgtctt ggcagggtga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
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attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480  
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540  
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600  
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggaggtg 660  
cataatgcca agacaaagcc gcgaggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720  
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caagggtctcc 780  
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900  
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960  
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cgggtccttc 1020  
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080  
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 <213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence: L104E1g  
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Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45

20

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60

25

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95

30

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125

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Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
 145 150 155 160

40

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val  
 165 170 175

45

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
 195 200 205

50

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 225 230 235 240

55

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
 260 265 270

5 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
 275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 290 295 300

10 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 305 310 315 320

15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
 340 345 350

20 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 370 375 380

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 <210> 3  
 <211> 1152  
 <212> DNA

30 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: L104EA29YIg  
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 ggcacgcgta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180  
 40 acagtgtctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
 gagctcatgt acccaccgcc atactacgag ggcataaggca acggaaccca gatttatgta 420  
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480  
 45 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540  
 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600  
 gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg 660  
 cataatgcc aagacaaagcc gcgaggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720  
 gtcttcaccg tcttcacca ggactgggtg aatggcaagg agtacaagtg caagggtctcc 780  
 50 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
 gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900  
 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960  
 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020  
 ttctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080  
 55 tgctcogtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140  
 ccgggtaaat ga 1152

<210> 4  
 <211> 383  
 <212> PRT  
 5 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: L104EA29YIg  
 sequence

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 15 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30  
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 20 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95  
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125  
 35 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140  
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
 145 150 155 160  
 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val  
 165 170 175  
 45 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 180 185 190  
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
 195 200 205  
 50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 210 215 220  
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 225 230 235 240  
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

245

250

255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
260 265 270

5

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
275 280 285

10

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
305 310 315 320

15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
340 345 350

20

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

25

&lt;210&gt; 5

&lt;211&gt; 1152

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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<223> Description of Artificial Sequence: L104EA29LIg  
sequence

&lt;400&gt; 5

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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtagctgc cagcagccga 120  
40 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aattgactga ggtccgggtg 180  
acagtgtctt ggcaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420  
45 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480  
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540  
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600  
gacgtgagcc acgaagaccc tgaggtcaaag ttcaactggg acgtggacgg cgtggagggtg 660  
cataatgcc aagacaaagcc ggggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720  
50 gtcctcaccg tcttcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780  
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
gaaccacagg tgtacacct gcccccattc cgggatgagc tgaccaagaa ccaggtcagc 900  
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagtgcaat 960  
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020  
55 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080  
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ccgggtaaat ga 1152

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 <211> 383  
 <212> PRT  
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: L104EA29LIg  
 sequence

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 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
 1 5 10 15  
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30  
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 Tyr Ala Ser Pro Gly Lys Leu Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95  
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125  
 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140  
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
 145 150 155 160  
 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val  
 165 170 175  
 45 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 180 185 190  
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
 195 200 205  
 50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 210 215 220  
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
305 310 315 320

15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

<210> 7

30 <211> 1152

<212> DNA

<213> Artificial Sequence

<220>

35 <223> Description of Artificial Sequence: L104EA29TIg  
sequence

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acagtgtctt gccaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
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45 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420  
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acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540  
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600  
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg 660  
50 cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720  
gtcctcaccg tcttgacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780  
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900  
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5 <210> 8  
 <211> 383  
 <212> PRT  
 <213> Artificial Sequence

10 <220>  
 <223> Description of Artificial Sequence: L104EA29TIg  
 sequence

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 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30  
 20 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 Tyr Ala Ser Pro Gly Lys Thr Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95  
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 35 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125  
 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140  
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
 145 150 155 160  
 45 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val  
 165 170 175  
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 180 185 190  
 50 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
 195 200 205  
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 210 215 220  
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 225 230 235 240



Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
290 295 300

15 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

30 <210> 9  
<211> 1152  
<212> DNA  
<213> Artificial Sequence

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ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatggactga ggtccgggtg 180  
acagtgttcc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttcc agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
45 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420  
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50 gacgtgagcc acgaagacc tgaggtaag ttcaactgg acgtggacgg cgtggaggtg 660  
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720  
gtcctcaccg tctgcacca ggactggctg aatggcaagg agtacaagt caaggtctcc 780  
aacaagccg tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggctcagc 900  
55 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960  
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1020  
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080

tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140  
ccgggtaaat ga 1152

5 <210> 10  
<211> 383  
<212> PRT  
<213> Artificial Sequence

10 <220>  
<223> Description of Artificial Sequence: L104EA29Wlg  
sequence

<400> 10

15 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
1 5 10 15  
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
20 25 30  
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
35 40 45  
25 Tyr Ala Ser Pro Gly Lys Trp Thr Glu Val Arg Val Thr Val Leu Arg  
50 55 60  
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
65 70 75 80  
30 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95  
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110  
35 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
115 120 125  
Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
40 130 135 140  
Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
145 150 155 160  
45 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val  
165 170 175  
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
180 185 190  
50 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
195 200 205  
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
55 210 215 220  
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
245 250 255

5

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
260 265 270

10

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
290 295 300

15

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
325 330 335

20

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
340 345 350

25

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

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<210> 11  
<211> 636  
<212> DNA  
<213> Homo sapiens

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<400> 11  
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ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180  
40 acagtgcctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttccct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420  
attgatccag aaccgtgccc agattctgac ttctctctct ggatccttgc agcagttagt 480  
45 tcgggggttg ttttttatag ctttctctct acagctgttt ctttgagcaa aatgctaaag 540  
aaaagaagcc ctcttacaac aggggtctat gtgaaaatgc cccaacaga gccagaatgt 600  
gaaaagcaat ttcagcctta ttttattccc atcaat 636

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<210> 12  
<211> 212  
<212> PRT  
<213> Homo sapiens

55

<400> 12  
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30

5 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60

10 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80

15 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110

20 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140

25 Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser  
 145 150 155 160

30 Ser Gly Leu Phe Phe Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser  
 165 170 175

Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys  
 180 185 190

35 Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe  
 195 200 205

Ile Pro Ile Asn  
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<210> 13

<211> 1152

<212> DNA

45 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CTLA4Ig  
 sequence

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<400> 13

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 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180  
 55 acagtgttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
 ggggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360

gagctcatgt acccaccgcc atactacctg ggcataaggca acggaaccca gatttatgta 420  
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480  
 acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagtctt cctcttcccc 540  
 ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600  
 5 gacgtgagcc acgaagaccc tgaggtoaag ttcaactggt acgtggacgg cgtgggagtg 660  
 cataatgccca agacaaagcc gcgaggaggag cagtacaaca gcacgtaccg ggtggtcagc 720  
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780  
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840  
 10 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900  
 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960  
 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020  
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<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CTLA4Ig  
sequence

<400> 14

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His  
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val

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165 170 175

5 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
195 200 205

10 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
225 230 235 240

15 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile  
260 265 270

20 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
275 280 285

25 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
305 310 315 320

30 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
325 330 335

35 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
355 360 365

40 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

45 <210> 15  
<211> 6  
<212> PRT  
<213> Homo sapiens

50 <400> 15  
Met Tyr Pro Pro Pro Tyr  
1 5

55 <210> 16  
<211> 65  
<212> DNA  
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<220>

<223> Description of Artificial Sequence: primer  
sequence encoding Oncostatin M-CTLA4 fusion

5 <400> 16  
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cagcc 65

10 <210> 17  
<211> 33  
<212> DNA  
<213> Artificial Sequence

15 <220>  
<223> Description of Artificial Sequence: primer  
sequence encoding CTLA4 sequence

20 <400> 17  
tttgggctcc tgatcagaat ctgggcacgg ttg 33

25 <210> 18  
<211> 72  
<212> DNA  
<213> Artificial Sequence

30 <220>  
<223> Description of Artificial Sequence: primer  
sequence encoding Oncostatin M signal peptide  
sequence

35 <400> 18  
ctagccactg aagcttcacc aatgggtgta ctgctcacac agaggacgct gtcagtctg 60  
gtccttgcaac tc 72

40 <210> 19  
<211> 41  
<212> DNA  
<213> Artificial Sequence

45 <220>  
<223> Description of Artificial Sequence: primer  
sequence from vector sequence

<400> 19  
gaggtgataa agcttcacca atgggtgtac tgctcacaca g 41

50 <210> 20  
<211> 42  
<212> DNA  
<213> Artificial Sequence

55 <220>  
<223> Description of Artificial Sequence: primer

sequence encoding CTLA4 sequence

<400> 20

gtggtgtatt ggtctagatc aatcagaatc tgggcacggt tc

42

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